does not exclude the fact that equivalent proteins capable of being purified according to the process indicated above can have a slightly different N-terminal sequence, since they may be derived from another bacterial strain. Such a difference would indeed reflect the phenomenon of allelic variance commonly encountered within the same species. For example, a bacterial species is usually represented by a group of strains which differ from each other in minor allelic characteristics. A polypeptide which fulfils the same biological function in different strains may have an amino acid sequence which is not different for all the strains. Such an allelic variation also exists in DNA.

Insert the following phrase as a new line on page 20, after line 22 and before line 23:

BRIEF DESCRIPTION OF THE DRAWINGS

Replace the paragraph on page 31, lines 3-5 with the following new paragraph, which adds a sequence identification number after the amino acid sequence in this paragraph:

(iii) A monomeric form at 54 kDa in SDS-PAGE with the following N-terminal sequence: MVNKDVKQTTAFGAPVWDDNNVITAGPRG (SEQ ID NO: 2).

Replace line 20 on page 37 with the following new line, which corrects the sequence identification number in this line:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

In the Claims:

Cancel claims 2, 8, 9, 12, and 13, and amend claims 1, 3-7, 10, 11, and 14-16 as follows.

1. (Amended) A composition consisting essentially of a *Helicobacter pylori* membrane fraction protein in a pharmaceutically acceptable form, wherein said protein has a molecular weight that appears to be of the order of 50, 32-35, or 30 kDa after electrophoresis on a 10% polyacrylamide gel in the presence of SDS.